RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _09/920,137G_

Source: _1Fw/6,_

Date Processed by STIC: _1/19/06_

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IFW16

RAW SEQUENCE LISTING   DATE: 01/19/2006
PATENT APPLICATION: US/09/920,137G   TIME: 12:23:51

Input Set : N:\SMITH\PTO.TS18.txt
Output Set: N:\CRF4\01192006\I920137G.raw

```
 5 <110> APPLICANT: Giles-Komar, Jill; David Shealy; David Knight; Bernie
 6         Scallon; George Heavner
 8 <120> TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
10 <130> FILE REFERENCE: CEN0250 NP
12 <140> CURRENT APPLICATION NUMBER: US 09/920,137G
13 <141> CURRENT FILING DATE: 2001-08-01
15 <150> PRIOR APPLICATION NUMBER: 60/223,360
16 <151> PRIOR FILING DATE: 2000-08-07
18 <150> PRIOR APPLICATION NUMBER: 60/236,826
19 <151> PRIOR FILING DATE: 2000-09-29
21 <160> NUMBER OF SEQ ID NOS: 35
23 <170> SOFTWARE: PatentIn Ver 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 5
27 <212> TYPE: PRT
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: MISC_FEATURE
32 <222> LOCATION: (1)..(5)
33 <223> OTHER INFORMATION: Heavy Chain complementarity determinng region 1 (CDR1).
36 <400> SEQUENCE: 1
38   Ser Tyr Ala Met His
39   1               5
42 <210> SEQ ID NO: 2
43 <211> LENGTH: 17
44 <212> TYPE: PRT
45 <213> ORGANISM: Homo sapiens
47 <220> FEATURE:
48 <221> NAME/KEY: MISC_FEATURE
49 <222> LOCATION: (1)..(17)
50 <223> OTHER INFORMATION: Heavy Chain complementarity determinng region 2 (CDR2).
52 <220> FEATURE:
53 <221> NAME/KEY: MISC_FEATURE
54 <222> LOCATION: (1)..(1)
55 <223> OTHER INFORMATION: Xaa at position 1 is selected from Ile, Phe or Val.
57 <220> FEATURE:
58 <221> NAME/KEY: MISC_FEATURE
59 <222> LOCATION: (2)..(2)
60 <223> OTHER INFORMATION: Xaa at position 2 is selected from Ile or Met.
62 <220> FEATURE:
63 <221> NAME/KEY: MISC_FEATURE
64 <222> LOCATION: (3)..(3)
65 <223> OTHER INFORMATION: Xaa at position 3 is selected from Ser or Leu.
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 67 <220> FEATURE:
 68 <221> NAME/KEY: MISC_FEATURE
 69 <222> LOCATION: (4)..(4)
 70 <223> OTHER INFORMATION: Xaa at position 4 is selected from Tyr or Phe.
 72 <220> FEATURE:
 73 <221> NAME/KEY: MISC_FEATURE
 74 <222> LOCATION: (10)..(10)
 75 <223> OTHER INFORMATION: Xaa at position 10 is selected from Lys or Tyr.
 77 <220> FEATURE:
 78 <221> NAME/KEY: MISC_FEATURE
 79 <222> LOCATION: (11)..(11)
 80 <223> OTHER INFORMATION: Xaa at position 11 is selected from Ser or Tyr.
 82 <220> FEATURE:
 83 <221> NAME/KEY: MISC_FEATURE
 84 <222> LOCATION: (17)..(17)
 85 <223> OTHER INFORMATION: Xaa at position 17 is selected from Asp or Gly.
 88 <400> SEQUENCE: 2
W--> 90  Xaa Xaa Xaa Xaa Asp Gly Ser Asn Lys Xaa Xaa Ala Asp Ser Val Lys Xaa
 91      1               5                  10                  15
 93 <210> SEQ ID NO: 3
 94 <211> LENGTH: 17
 95 <212> TYPE: PRT
 96 <213> ORGANISM: Homo sapiens
 98 <220> FEATURE:
 99 <221> NAME/KEY: MISC_FEATURE
100 <222> LOCATION: (1)..(17)
101 <223> OTHER INFORMATION: Heavy Chain complementarity determinng region 3 (CDR3).
103 <220> FEATURE:
104 <221> NAME/KEY: MISC_FEATURE
105 <222> LOCATION: (4)..(4)
106 <223> OTHER INFORMATION: Xaa at position 4 is selected from Ile or Val.
108 <220> FEATURE:
109 <221> NAME/KEY: MISC_FEATURE
110 <222> LOCATION: (5)..(5)
111 <223> OTHER INFORMATION: Xaa at position 5 is selected from Ser, Ala or Gly.
113 <220> FEATURE:
114 <221> NAME/KEY: MISC_FEATURE
115 <222> LOCATION: (9)..(9)
116 <223> OTHER INFORMATION: Xaa at position 9 is selected from Asn or Tyr.
118 <400> SEQUENCE: 3
W--> 120  Asp Arg Gly Xaa Xaa Ala Gly Gly Xaa Tyr Tyr Tyr Tyr Gly Met Asp Val
121   1               5                  10                  15
123 <210> SEQ ID NO: 4
124 <211> LENGTH: 11
125 <212> TYPE: PRT
126 <213> ORGANISM: Homo sapiens
128 <220> FEATURE:
129 <221> NAME/KEY: MISC_FEATURE
130 <222> LOCATION: (1)..(11)
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131 <223> OTHER INFORMATION: Light Chain complementarity determinng region 1 (CDR1).
133 <220> FEATURE:
134 <221> NAME/KEY: MISC_FEATURE
135 <222> LOCATION: (7)..(7)
136 <223> OTHER INFORMATION: Xaa at position 7 is selected from Ser or Tyr.
138 <400> SEQUENCE: 4
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W--> **140 Arg Ala Ser Gln Ser Val Xaa Ser Tyr Leu Ala**
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141  1               5                   10
143 <210> SEQ ID NO: 5
144 <211> LENGTH: 7
145 <212> TYPE: PRT
146 <213> ORGANISM: Homo sapiens
149 <220> FEATURE:
150 <221> NAME/KEY: MISC_FEATURE
151 <222> LOCATION: (1)..(7)
152 <223> OTHER INFORMATION: Light Chain complementarity determinng region 2 (CDR2).
154 <400> SEQUENCE: 5
156  Asp Ala Ser Asn Arg Ala Thr
157  1               5
159 <210> SEQ ID NO: 6
160 <211> LENGTH: 10
161 <212> TYPE: PRT
162 <213> ORGANISM: Homo sapiens
164 <220> FEATURE:
165 <221> NAME/KEY: MISC_FEATURE
166 <222> LOCATION: (1)..(10)
167 <223> OTHER INFORMATION: Light Chain complementarity determinng region 3 (CDR3).
169 <400> SEQUENCE: 6
171  Gln Gln Arg Ser Asn Trp Pro Pro Phe Thr
172  1               5                   10
174 <210> SEQ ID NO: 7
175 <211> LENGTH: 126
176 <212> TYPE: PRT
177 <213> ORGANISM: Homo sapiens
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W--> **178 <400> SEQUENCE: 7**
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180 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
181 1               5                   10                  15
183 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr
184             20                  25                  30
186 Ala Met His Trp Val Arg Gln Ala Pro Gly Asn Gly Leu Glu Trp Val
187         35                  40                  45
189 Ala Phe Met Ser Tyr Asp Gly Ser Asn Lys Lys Tyr Ala Asp Ser Val
190     50                  55                  60
192 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
193 65                  70                  75                  80
195 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
196             85                  90                  95
198 Ala Arg Asp Arg Gly Ile Ala Ala Gly Gly Asn Tyr Tyr Tyr Tyr Gly
199             100                 105                 110
```

```
201 Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
202         115                 120             125
206 <210> SEQ ID NO: 8
207 <211> LENGTH: 108
208 <212> TYPE: PRT
209 <213> ORGANISM: Homo sapiens
W--> 210 <400> SEQUENCE: 8
212 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
213 1               5                 10                 15
215 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Tyr Ser Tyr
216             20                 25                 30
218 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
219         35                 40                 45
221 Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
222     50                 55                 60
224 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
225 65                 70                 75                 80
227 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
228             85                 90                 95
230 Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
231             100                 105
234 <210> SEQ ID NO: 9
235 <211> LENGTH: 157
236 <212> TYPE: PRT
237 <213> ORGANISM: Homo sapiens
239 <220> FEATURE:
240 <221> NAME/KEY: MISC_FEATURE
241 <222> LOCATION: (1)..(157)
242 <223> OTHER INFORMATION: human TNF alpha monomer sequence
244 <400> SEQUENCE: 9
246 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
247 1               5                 10                 15
249 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
250             20                 25                 30
252 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
253             35                 40                 45
255 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
256     50                 55                 60
258 Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
259 65                 70                 75                 80
261 Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
262             85                 90                 95
264 Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
265             100                 105                 110
267 Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
268             115                 120                 125
270 Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
271         130                 135                 140
273 Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
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        Input Set : N:\SMITH\PTO.TS18.txt
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274 145   150   155
276 <210> SEQ ID NO: 10
277 <211> LENGTH: 18
278 <212> TYPE: DNA
279 <213> ORGANISM: Homo sapiens
281 <400> SEQUENCE: 10
283   ttggtccagt cggactgg   18
285 <210> SEQ ID NO: 11
286 <211> LENGTH: 18
287 <212> TYPE: DNA
288 <213> ORGANISM: Homo sapiens
290 <400> SEQUENCE: 11
292   cacctgcact cggtgctt   18
294 <210> SEQ ID NO: 12
295 <211> LENGTH: 30
296 <212> TYPE: DNA
297 <213> ORGANISM: Homo sapiens
299 <400> SEQUENCE: 12
301   cactgttttg agtgtgtacg ggcttaagtt   30
303 <210> SEQ ID NO: 13
304 <211> LENGTH: 18
305 <212> TYPE: DNA
306 <213> ORGANISM: Homo sapiens
308 <400> SEQUENCE: 13
310   gccgcacgtg tggaaggg   18
312 <210> SEQ ID NO: 14
313 <211> LENGTH: 25
314 <212> TYPE: DNA
315 <213> ORGANISM: Homo sapiens
317 <400> SEQUENCE: 14
319   agtcaaggtc ggactggctt aagtt   25
321 <210> SEQ ID NO: 15
322 <211> LENGTH: 28
323 <212> TYPE: DNA
324 <213> ORGANISM: Homo sapiens
326 <400> SEQUENCE: 15
328   gttgtcccct ctcacaatct tcgaattt   28 ·
330 <210> SEQ ID NO: 16
331 <211> LENGTH: 18
332 <212> TYPE: DNA
333 <213> ORGANISM: Homo sapiens
335 <400> SEQUENCE: 16
337   ggcggtagac tactcgtc   18
340 <210> SEQ ID NO: 17
341 <211> LENGTH: 7
342 <212> TYPE: PRT
343 <213> ORGANISM: Homo sapiens
345 <400> SEQUENCE: 17
347 Met Asp Trp Thr Trp Ser Ile

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 01/19/2006
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 1,2,3,4,10,11,17
Seq#:3; Xaa Pos. 4,5,9
Seq#:4; Xaa Pos. 7

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:32; Line(s) 490
Seq#:33; Line(s) 508
Seq#:34; Line(s) 528
Seq#:35; Line(s) 550

VERIFICATION SUMMARY　　　　　　　　DATE: 01/19/2006
PATENT APPLICATION:　**US/09/920,137G**　　TIME: 12:23:52

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L:90 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:178 M:283 W: Missing Blank Line separator, <400> field identifier
L:210 M:283 W: Missing Blank Line separator, <400> field identifier